

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2005, 23:19:26 ; Search time 26 Seconds
(without alignments)
1564.478 Million cell updates/sec

Perfect score: 2527
Sequence: 1 MVKFPALHYWFLRFLVPL.....TDMPTTEVTDIVRENE 492

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/PGTUS_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
3	1063	42.1	207	2	US-09-489-847-320
4	812	32.1	162	2	US-09-489-847-160
5	586	23.2	114	2	US-09-489-847-321
6	118.5	4.7	518	2	US-09-134-001C-4744
7	114.5	4.5	329	2	US-09-902-540-15354
8	109.5	4.3	610	2	US-08-970-725-2
9	108.5	4.3	361	2	US-09-196-520-6
10	104.5	4.1	610	1	US-08-212-188-2
11	104.5	4.1	610	4	PCT-US95-02708-2
12	104	4.1	536	2	US-09-107-532A-5507
13	103	4.1	631	2	US-09-107-532A-3902
14	103	4.1	1058	1	US-08-687-289A-5
15	103	4.1	1058	1	US-09-435-897-5
16	101.5	4.0	677	2	US-09-543-681A-6388
17	100.5	4.0	413	2	US-09-540-236-3672
18	100.5	4.0	411	2	US-10-104-047-3865
19	100	4.0	644	2	US-09-252-991A-21730
20	99	3.9	563	2	US-09-949-016-10317
21	99	3.9	584	2	US-09-693-746-22
22	98.5	3.9	472	2	US-09-934-899-10
23	98.5	3.9	472	2	US-09-934-868-30
24	98.5	3.9	472	2	US-10-701-200-30
25	98.5	3.9	513	2	US-09-303-518D-582
26	98.5	3.9	516	2	US-09-252-991A-21329
27	98	3.9	534	2	US-09-328-352-6713
28	98	3.9	619	2	US-09-540-236-2377
29	96.5	3.8	509	2	US-09-252-991A-30864
30	96.5	3.8	513	2	US-09-303-518D-580

31	96.5	3.8	528	1	US-08-403-852D-21	Sequence 21, Appl
32	96.5	3.8	528	2	US-08-510-646B-22	Sequence 22, Appl
33	96.5	3.8	528	2	US-09-231-818-21	Sequence 21, Appl
34	96.5	3.8	528	2	US-09-635-359B-21	Sequence 21, Appl
35	96.5	3.8	808	2	US-09-134-001C-3105	Sequence 3105, Ap
36	96.5	3.8	962	2	US-09-328-352-7942	Sequence 7942, Ap
37	95.5	3.8	3287	1	US-08-477-451-7	Sequence 7, Appl
38	95	3.8	456	2	US-10-169-048-8	Sequence 8, Appl
39	95	3.8	768	2	US-09-489-039A-12897	Sequence 12897, A
40	94.5	3.8	801	2	US-09-710-279-2020	Sequence 2020, Ap
41	94	3.7	359	2	US-09-828-523A-14	Sequence 14, Appl
42	94	3.7	370	2	US-09-828-523A-74	Sequence 74, Appl
43	94	3.7	450	2	US-09-252-991A-28134	Sequence 28134, A
44	93.5	3.7	350	1	US-07-759-568-3	Sequence 3, Appl
45	93.5	3.7	364	2	US-09-196-520-9	Sequence 9, Appl
46	93.5	3.7	551	2	US-09-615-192A-348	Sequence 348, App
47	93.5	3.7	565	2	US-09-489-039A-8414	Sequence 8414, Ap
48	93.5	3.7	1607	2	US-09-902-540-16765	Sequence 16765, A
49	93	3.7	449	2	US-09-328-352-7512	Sequence 7512, Ap
50	93	3.7	474	2	US-09-489-039A-11844	Sequence 11844, A
51	93	3.7	493	2	US-09-134-001C-3486	Sequence 3486, Ap
52	92.5	3.7	1065	2	US-09-252-991A-31637	Sequence 31637, A
53	92.5	3.7	407	2	US-09-769-787-14	Sequence 14, Appl
54	92.5	3.7	466	2	US-09-489-039A-13781	Sequence 12781, A
55	92.5	3.7	513	2	US-09-489-039A-12877	Sequence 12877, A
56	92	3.6	315	1	US-08-118-270-34	Sequence 34, Appl
57	92	3.6	483	2	US-09-134-000C-4234	Sequence 4234, Ap
58	91.5	3.6	318	2	US-09-489-039A-10467	Sequence 8, Appl
59	91.5	3.6	350	2	US-08-430-286A-8	Sequence 7659, Ap
60	91.5	3.6	451	2	US-09-328-352-7659	Sequence 3651, Ap
61	91.5	3.6	456	2	US-09-583-110-3651	Sequence 5001, Ap
62	91.5	3.6	460	2	US-09-107-433-5001	Sequence 27411, A
63	91.5	3.6	375	2	US-09-252-991A-27411	Sequence 305, App
64	91	3.6	454	2	US-09-489-847-305	Sequence 426, App
65	91	3.6	467	2	US-09-198-452A-443	Sequence 10085, A
66	91	3.6	479	2	US-09-438-185A-426	Sequence 19270, A
67	91	3.6	487	2	US-09-902-540-10085	Sequence 52, Appl
68	91	3.6	542	2	US-09-252-991A-19270	Sequence 11138, A
69	91	3.6	675	2	US-09-533-029-52	Sequence 5694, Ap
70	90.5	3.6	312	2	US-09-489-039A-11138	Sequence 2206, Ap
71	90.5	3.6	448	2	US-09-328-352-5694	Sequence 11, Appl
72	90.5	3.6	457	2	US-09-107-532A-4534	Sequence 18036, A
73	90.5	3.6	557	2	US-09-540-236-2206	Sequence 3, Appl
74	90.5	3.6	595	1	US-08-677-049-11	Sequence 6, Appl
75	90.5	3.6	638	2	US-09-252-991A-18036	Sequence 6, Appl
76	90.5	3.6	363	1	US-08-148-209A-3	Sequence 6, Appl
77	90	3.6	431	2	US-09-549-848B-6	Sequence 6, Appl
78	90	3.6	431	2	US-09-688-089-6	Sequence 16824, A
79	90	3.6	502	2	US-09-248-796A-16824	Sequence 499, App
80	90	3.6	502	2	US-09-826-509-499	Sequence 3842, Ap
81	89.5	3.5	453	2	US-09-583-110-3842	Sequence 3722, Ap
82	89.5	3.5	461	2	US-09-107-433-3722	Sequence 16249, A
83	89.5	3.5	482	2	US-09-902-540-16249	Sequence 626, App
84	89.5	3.5	594	2	US-09-605-703B-626	Sequence 6, Appl
85	89.5	3.5	1528	1	US-08-463-092B-6	Sequence 6, Appl
86	89.5	3.5	1528	1	US-08-460-907B-6	Sequence 6, Appl
87	89.5	3.5	1528	2	US-08-463-179A-6	Sequence 6, Appl
88	89.5	3.5	1528	2	US-08-461-384B-6	Sequence 6643, Ap
89	89.5	3.5	316	2	US-09-107-532A-6643	Sequence 10560, A
90	89.5	3.5	433	2	US-09-252-991A-3726	Sequence 23726, A
91	89	3.5	316	2	US-09-489-039A-10560	Sequence 4956, Ap
92	89	3.5	458	2	US-09-583-110-2977	Sequence 4956, Ap
93	89	3.5	319	2	US-09-107-433-4956	Sequence 19033, A
94	88.5	3.5	341	2	US-09-252-991A-19033	Sequence 4006, Ap
95	88.5	3.5	409	2	US-09-107-532A-4006	Sequence 5459, Ap
96	88.5	3.5	420	2	US-09-107-532A-5459	Sequence 1, Appl
97	88.5	3.5	424	2	US-09-178-093B-1	Sequence 93, Appl
98	88.5	3.5	466	2	US-09-800-729-93	Sequence 180, App
99	88.5	3.5	509	2	US-09-800-729-180	Sequence 5305, Ap
100	88.5	3.5	526	2	US-09-543-681A-5305	Sequence 9805, Ap
101	88.5	3.5	401	2	US-09-489-039A-9805	
102	88	3.5	426	2		
103	88	3.5				

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OM protein - protein search, using sw model

Run on: December 3, 2005, 23:20:36 ; Search time 71 Seconds
(without alignments)

Perfect score: 2527
Sequence: 1 MVKPPALHYVPLIRFLVPL.....TDMPTTEVTDIVENRENE 492
2895.381 Million cell updates/sec

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

Published Applications AA_Main:

1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pep.*

2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep.*

3: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep.*

4: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pep.*

5: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pep.*

6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match		Length	DB ID	Description
		Match	%			
35	2527	100.0		492	4	US-10-167-749-7
45	2527	100.0		492	4	US-10-210-951-16
47	2527	100.0		492	4	US-10-211-884-16
73	2527	100.0		492	4	US-10-170-481A-7
75	2527	100.0		492	4	US-10-210-028-7
80	2527	100.0		492	4	US-10-162-521A-7
81	2527	100.0		492	4	US-10-211-858-16
93	2527	100.0		492	5	US-10-918-851-7
94	2527	100.0		492	5	US-10-805-667-7
95	2527	100.0		492	5	US-10-897-359-7
96	2527	100.0		492	5	US-10-893-802-7
97	2527	100.0		492	5	US-10-897-360-7
98	2527	100.0		492	5	US-10-367-057-48
100	2527	100.0		492	6	US-11-129-762-7
101	2522	99.8		492	5	US-10-169-596A-2
102	2522	99.8		492	5	US-10-489-125B-3
103	2502	99.0		492	5	US-10-169-596A-16
104	2285	90.4		445	4	US-10-839-882-8
105	1396.5	55.3		306	5	US-10-450-763-40695
106	1162	46.0		459	5	US-10-450-763-40696
107	1063	42.1		207	4	US-10-351-334-320
108	1049	41.5		205	4	US-10-264-237-2336
109	812	32.1		161	5	US-10-472-533-388
110	812	32.1		162	4	US-10-351-334-160
111	586	23.2		114	4	US-10-351-334-321
112	256	10.1		47	3	US-09-864-761-40397
113	193	7.6		40	3	US-09-864-761-41066
114	122.5	4.8		512	4	US-10-161-493-36

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OM protein - protein search, using sw model

Run on: December 3, 2005, 23:20:47 ; Search time 7 Seconds

(without alignments)

336.551 Million cell updates/sec

Perfect score: 2527

Sequence: 1 MVKFPALTHYKPLRLVPL.....TDMPTREVTDIVMRSENE 492

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 26661 seqs, 4788334 residues

Total number of hits satisfying chosen parameters: 26661

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : Published Applications AA New:

- 1: /cgm2_6/ptodata/1/pubaa/US09_NEW_PUB pep.*
- 2: /cgm2_6/ptodata/1/pubaa/US06_NEW_PUB pep.*
- 3: /cgm2_6/ptodata/1/pubaa/US07_NEW_PUB pep.*
- 4: /cgm2_6/ptodata/1/pubaa/US08_NEW_PUB pep.*
- 5: /cgm2_6/ptodata/1/pubaa/PCT_NEW_PUB pep.*
- 6: /cgm2_6/ptodata/1/pubaa/US10_NEW_PUB pep.*
- 7: /cgm2_6/ptodata/1/pubaa/US11_NEW_PUB pep.*
- 8: /cgm2_6/ptodata/1/pubaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	117.5	4.6	693	6	US-10-467-657-6176
2	99	3.9	563	6	US-10-821-234-1090
3	98.5	3.9	486	6	US-10-467-657-950
4	98	3.9	490	7	US-11-074-176-316
5	98	3.9	495	7	US-11-074-176-60
6	95	3.8	501	7	US-11-055-822-52
7	94.5	3.7	801	6	US-10-793-626-2020
8	90	3.6	431	7	US-11-092-140-6
9	89.5	3.5	984	7	US-11-055-822-508
10	89.5	3.5	984	6	US-11-055-822-594
11	89	3.5	321	6	US-10-467-657-2352
12	89	3.5	674	6	US-10-467-657-6812
13	87.5	3.5	433	7	US-11-082-389-332
14	84	3.3	354	6	US-10-821-234-1618
15	84	3.3	489	6	US-10-858-730-198
16	84	3.3	489	7	US-11-055-822-1152
17	82.5	3.3	342	6	US-10-793-626-2854
18	82.5	3.3	858	7	US-11-077-550-22
19	82.5	3.3	860	7	US-11-077-550-175
20	82.5	3.3	862	7	US-11-077-550-94
21	82.5	3.3	862	7	US-11-077-550-171
22	82.5	3.3	862	7	US-11-077-550-173
23	82.5	3.3	864	7	US-11-077-550-102
24	82.5	3.3	865	7	US-11-077-550-100
25	82.5	3.3	866	7	US-11-077-550-88
26	82.5	3.3	866	7	US-11-077-550-104

27	82.5	3.3	867	7	US-11-077-550-80	Sequence 80, Appl
28	82.5	3.3	867	7	US-11-077-550-96	Sequence 96, Appl
29	82.5	3.3	867	7	US-11-077-550-98	Sequence 98, Appl
30	82.5	3.3	870	7	US-11-077-550-92	Sequence 92, Appl
31	82.5	3.3	871	7	US-11-077-550-84	Sequence 84, Appl
32	82.5	3.3	871	7	US-11-077-550-86	Sequence 86, Appl
33	82.5	3.3	871	7	US-11-077-550-90	Sequence 90, Appl
34	82.5	3.3	876	7	US-11-077-550-82	Sequence 82, Appl
35	82.5	3.3	876	7	US-11-077-550-106	Sequence 106, Appl
36	82.5	3.3	876	7	US-11-077-550-108	Sequence 108, Appl
37	82.5	3.3	888	7	US-11-077-550-112	Sequence 112, Appl
38	82.5	3.3	1070	7	US-11-062	Sequence 4, Appl
39	82.5	3.3	1095	7	US-11-062	Sequence 7, Appl
40	82.5	3.3	1169	7	US-11-077-550-20	Sequence 20, Appl
41	82.5	3.3	1420	7	US-11-077-550-110	Sequence 110, Appl
42	81.5	3.2	205	6	US-10-793-626-2184	Sequence 2184, Ap
43	81	3.2	502	6	US-10-467-657-7332	Sequence 7332, Ap
44	80.5	3.2	372	6	US-10-467-657-590	Sequence 590, Appl
45	80	3.2	842	6	US-10-645-441-2	Sequence 2, Appl
46	79.5	3.1	360	6	US-10-858-730-110	Sequence 110, Appl
47	79.5	3.1	391	7	US-11-082-389-172	Sequence 172, Appl
48	79	3.1	196	6	US-10-485-517-420	Sequence 420, Appl
49	78.5	3.1	291	6	US-10-467-657-3890	Sequence 3890, Ap
50	78.5	3.1	322	7	US-11-082-389-188	Sequence 188, Appl
51	78.5	3.1	363	6	US-10-793-626-302	Sequence 302, Appl
52	78.5	3.1	391	7	US-11-082-389-174	Sequence 174, Appl
53	78.5	3.1	539	6	US-10-467-657-3146	Sequence 3146, Ap
54	78	3.1	307	7	US-11-055-822-834	Sequence 834, Appl
55	78	3.1	408	6	US-10-793-626-2286	Sequence 2286, Ap
56	76.5	3.0	393	7	US-11-092-140-2	Sequence 2, Appl
57	76.5	3.0	400	6	US-10-793-626-3116	Sequence 3116, Ap
58	76	3.0	506	6	US-10-485-517-344	Sequence 344, Appl
59	76	3.0	582	6	US-10-793-626-1080	Sequence 1080, Ap
60	75.5	3.0	540	6	US-10-485-517-223	Sequence 223, Appl
61	75.5	3.0	639	7	US-11-074-176-222	Sequence 222, Appl
62	75.5	3.0	637	7	US-11-082-389-362	Sequence 362, Appl
63	75	3.0	448	7	US-11-055-822-826	Sequence 826, Appl
64	75	3.0	455	7	US-11-102-240-4	Sequence 4, Appl
65	75	3.0	538	7	US-11-119-683-1	Sequence 1, Appl
66	75	3.0	1304	6	US-10-821-234-1648	Sequence 1648, Ap
67	74.5	2.9	394	6	US-10-392-234A-46	Sequence 46, Appl
68	74.5	2.9	394	6	US-10-392-234A-52	Sequence 52, Appl
69	74.5	2.9	407	6	US-10-821-234-1389	Sequence 1389, Ap
70	74.5	2.9	464	6	US-10-689-742-164	Sequence 164, Appl
71	74	2.9	368	7	US-11-082-389-320	Sequence 320, Appl
72	74	2.9	506	6	US-10-467-657-2088	Sequence 2088, Ap
73	74	2.9	585	7	US-11-012-762-6	Sequence 6, Appl
74	73.5	2.9	445	7	US-10-793-626-2644	Sequence 2644, Ap
75	73	2.9	304	7	US-11-082-389-14	Sequence 14, Appl
76	73	2.9	304	6	US-11-082-389-14	Sequence 14, Appl
77	73	2.9	450	6	US-10-467-657-2126	Sequence 2126, Ap
78	73	2.9	481	6	US-10-467-657-3124	Sequence 3124, Ap
79	73	2.9	481	6	US-10-467-657-6784	Sequence 6784, Ap
80	73	2.9	638	6	US-10-793-626-1468	Sequence 1468, Ap
81	73	2.9	739	7	US-11-082-389-94	Sequence 94, Appl
82	72.5	2.9	534	6	US-10-793-626-920	Sequence 920, Appl
83	72.5	2.9	914	6	US-10-467-657-638	Sequence 638, Appl
84	72	2.8	209	6	US-10-467-657-4066	Sequence 4066, Ap
85	72	2.8	350	6	US-10-502-145-1	Sequence 1, Appl
86	71.5	2.8	336	6	US-10-793-626-624	Sequence 624, Appl
87	71.5	2.8	336	6	US-10-793-626-2600	Sequence 2600, Ap
88	71.5	2.8	447	6	US-10-858-730-107	Sequence 107, Appl
89	71.5	2.8	447	6	US-10-858-730-107	Sequence 107, Appl
90	71.5	2.8	1167	6	US-10-942-072-13	Sequence 13, Appl
91	71	2.8	351	7	US-11-055-822-264	Sequence 264, Appl
92	71	2.8	367	7	US-11-055-822-262	Sequence 262, Appl
93	71	2.8	397	7	US-11-084-508-5	Sequence 5, Appl
94	71	2.8	432	7	US-11-055-822-1096	Sequence 1096, Ap
95	71	2.8	741	6	US-10-793-626-1178	Sequence 1178, Ap
96	71	2.8	741	6	US-10-858-730-199	Sequence 199, Appl
97	70.5	2.8	286	6	US-10-793-626-1008	Sequence 1008, Ap
98	70.5	2.8	291	6	US-10-793-626-2664	Sequence 2664, Ap
99	70.5	2.8	332	6	US-10-793-626-1008	Sequence 1008, Ap
100	70.5	2.8	521	6	US-10-793-626-532	Sequence 532, Appl
101	70.5	2.8	750	6	US-10-689-742-86	Sequence 86, Appl
102	70.5	2.8	928	6	US-10-841-129-4	Sequence 4, Appl